

SEQUENCE LISTING

<110> Moloney, Maurice  
Boothe, Joseph  
Rooijen, Gijs Van

<120> Oil Bodies and Associated Proteins as Affinity Matrices

<130> 9369-161

<140> US 09/707,167

<141> 2000-11-07

<150> US 09/319,275

<151> 1999-08-27

<160> 14

B<sup>2</sup> <170> PatentIn version 3.1

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Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile	
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Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val	
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Phe Ser Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser	
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Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr  
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Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu  
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Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile  
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Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile  
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35 40 45

Arg Gly Gly Gln His Thr Thr Ala Ile Glu Gly Arg Ile Thr Tyr Thr  
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Asp Cys Thr Glu Ser Gly Gln Asn Leu Cys Leu Cys Glu Gly Ser Asn  
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Val Cys Gly Lys Gly Asn Lys Cys Ile Leu Gly Ser Asn Gly Lys Gly  
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<222> (1092)..(1856)

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225 230 235	
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Val	Ile	Phe	Ser
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Leu	Ile	Thr	Val
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Gln	Asp	Ile	Lys
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Gly	Gln	Gln	His
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Gly	Glu	His	Asp
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Arg	Asp	Arg	Thr
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Gly	Gln	His	Thr
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Ser	Met	Asp	Pro
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Ser	Cys	Ala	Ala
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caa gct cca aaa gct gat gcg caa caa aat aac ttc aac aaa gat caa 145
Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln
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Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro
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aaa gct gat aac aat ttc aac aaa gaa caa caa aat gct ttc tat gaa 337
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cca agc caa agc gct aac ctt tta gca gaa gct aaa aag cta aat gat 625
Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp
                195          200          205

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Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala	
130 135 140	
Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn	
145 150 155 160	

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu  
165 170 175

Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro  
180 185 190

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala  
195 200 205

Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala  
210 215 220

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn  
225 230 235 240

Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Gly Asn Ser Arg Gly Ser  
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Val Asp Leu Gln Ile Thr Asn  
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tcgtcgggtc cttgggcgat tgcggcggaa gatgggtcag cttgggcttg aggacgagac 180  
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gagggtttgag ggaaaggaca aatgggtttg gctctggaga aagagagtgc ggcttttagag 300  
agagaattga gaggtttaga gagagatgcg gcggcgatga cgggaggaga gacgacgagg 360  
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Met Ala Asp Thr Ala Arg Gly Thr His  
1 5  
cac gat atc atc ggc aga gac cag tac ccg atg atg ggc cga gac cga 942  
His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg  
10 15 20 25  
gac cag tac cag atg tcc gga cga gga tct gac tac tcc aag tct agg 990  
Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg  
30 35 40  
cag att gct aaa gct gca act gct gtc aca gct ggt ggt tcc ctc ctt 1038  
Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu

45	50	55	
gtt ctc tcc agc ctt acc ctt gtt gga act gtc ata gct ttg act gtt Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val 60 65 70			1086
gca aca cct ctg ctc gtt atc ttc agc cca atc ctt gtc ccg gct ctc Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu 75 80 85			1134
atc aca gtt gca ctc ctc atc acc ggt ttt ctt tcc tct gga ggg ttt Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe 90 95 100 105			1182
ggc att gcc gct ata acc gtt ttc tct tgg att tac aagtaagcac Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile Tyr 110 115			1228
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gca acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg 120 125 130			1512
atg aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr 135 140 145 150			1560
tac gga cag caa cat act ggt ggg gaa cat gac cgt gac cgt act cgt Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr Arg 155 160 165			1608
ggt ggc cag cac act act ctc gtt cca cga gga tcc atg gat caa cgc Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Asp Gln Arg 170 175 180			1656
aat ggt ttt atc caa agc ctt aaa gat gat cca agc caa agt gct aac Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn 185 190 195			1704
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gat gcg caa caa aat aac ttc aac aaa gat caa caa agc gcc ttc tat Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe Tyr 215 220 225 230			1800
gaa atc ttg aac atg cct aac tta aac gaa gcg caa cgt aac ggc ttc Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe 235 240 245			1848
att caa agt ctt aaa gac gac cca agc caa agc act aac gtt tta ggt Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu Gly 250 255 260			1896
gaa gct aaa aaa tta aac gaa tct caa gca ccg aaa gct gat aac aat Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn 265 270 275			1944
ttc aac aaa gaa caa caa aat gct ttc tat gaa atc ttg aat atg cct Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro 280 285 290			1992

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gac cca agc caa agt gct aac cta ttg tca gaa gct aaa aag tta aat Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn 315 320 325	2088
gaa tct caa gca ccg aaa gcg gat aac aaa ttc aac aaa gaa caa caa Glu Ser Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln 330 335 340	2136
aat gct ttc tat gaa atc tta cat tta cct aac tta aac gaa gaa caa Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln 345 350 355	2184
cgc aat ggt ttc atc caa agc cta aaa gat gac cca agc caa agc gct Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala 360 365 370	2232
aac ctt tta gca gaa gct aaa aag cta aat gat gct caa gca cca aaa Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys 375 380 385 390	2280
gct gac aac aaa ttc aac aaa gaa caa caa aat gct ttc tat gaa att Ala Asp Asn Lys Phe Asn Lys Glu Gln Asn Ala Phe Tyr Glu Ile 395 400 405	2328
tta cat tta cct aac tta act gaa gaa caa cgt aac ggc ttc atc caa Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln 410 415 420	2376
agc ctt aaa gac gat ccg ggg aat tcc cgg gga tcc gtc gac ctg cag Ser Leu Lys Asp Asp Pro Gly Asn Ser Arg Gly Ser Val Asp Leu Gln 425 430 435	2424
ata aca aat tagaagcttg catgcctgca ggtcgatcgt tcaaacattt Ile Thr Asn 440	2473
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<212> PRT

<213> Artificial Sequence

<220>

<223> Oleosin - Protein A Fusion

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Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu 50 55 60		
Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile 65 70 75 80		
Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile 85 90 95		
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Phe Ser Trp Ile Tyr 115		
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Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr 35 40 45		
Arg Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Asp Gln 50 55 60		
Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala 65 70 75 80		
Asn Val Leu Gly Glu Ala Gln Lys Leu Asn Asp Ser Gln Ala Pro Lys 85 90 95		
Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe 100 105 110		



Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly  
115 120 125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu  
130 135 140

Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn  
145 150 155 160

Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met  
165 170 175

Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys  
180 185 190

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu  
195 200 205

Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln  
210 215 220

Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu  
225 230 235 240

Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser  
245 250 255

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro  
260 265 270

Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu  
275 280 285

Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile  
290 295 300

Gln Ser Leu Lys Asp Asp Pro Gly Asn Ser Arg Gly Ser Val Asp Leu  
305 310 315 320

Gln Ile Thr Asn